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Docket No. GEN-T111XC3D1

SEQUENCE LISTING

<110> Cohen, Daniel
Blumenfeld, Marta
Ilya, Chumakov
Bougueleret, Lydie

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Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly Met Leu Met Thr Asp
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gct gga agg aag ctg tat gtg aac acc tgg ata tat gga acc cta ctt      1062
Ala Gly Arg Lys Leu Tyr Val Asn Thr Trp Ile Tyr Gly Thr Leu Leu
330                               335                               340
ggc tgc ctg tgg gtt act att aaa gca tag acaagtagct gtctccagac      1112
Gly Cys Leu Trp Val Thr Ile Lys Ala *
345                               350
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acgaaagctg atatgcaatg gtcttgggca aacataacctg gttgtacaac tttagcatcg      1292
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<221> MYRISTATE
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<223> Prosite match

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<221> AMIDATION
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<221> PHOSPHORYLATION
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Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
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 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
 50 55 60
 Leu Tyr Gly Asp Leu Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala
 65 70 75 80
 Asn His Gln Ser Thr Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile
 85 90 95
 Arg Gln Asn Ala Leu Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu
 100 105 110
 Lys Trp Leu Pro Leu Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile
 115 120 125
 Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys
 130 135 140
 Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val Ile Phe
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 Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala
 165 170 175
 Ser Gln Ala Phe Ala Ala Gln Arg Gly Leu Ala Val Leu Lys His Val
 180 185 190
 Leu Thr Pro Arg Ile Lys Ala Thr His Val Ala Phe Asp Cys Met Lys
 195 200 205
 Asn Tyr Leu Asp Ala Ile Tyr Asp Val Thr Val Val Tyr Glu Gly Lys
 210 215 220
 Asp Asp Gly Gly Gln Arg Arg Glu Ser Pro Thr Met Thr Glu Phe Leu
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 Cys Lys Glu Cys Pro Lys Ile His Ile His Ile Asp Arg Ile Asp Lys
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 Lys Asp Val Pro Glu Glu Gln Glu His Met Arg Arg Trp Leu His Glu
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 275 280 285
 Asp Pro Glu Arg Arg Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys
 290 295 300
 Leu Ser Ile Lys Lys Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu
 305 310 315 320
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 20 25 30
 Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln
 35 40 45
 Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe
 50 55 60
 Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu Leu Tyr Gly Asp Leu

65					70					75					80
Pro	Lys	Asn	Lys	Glu	Asn	Ile	Ile	Tyr	Leu	Ala	Asn	His	Gln	Ser	Thr
				85					90					95	
Val	Asp	Trp	Ile	Val	Ala	Asp	Ile	Leu	Ala	Ile	Arg	Gln	Asn	Ala	Leu
			100					105					110		
Gly	His	Val	Arg	Tyr	Val	Leu	Lys	Glu	Gly	Leu	Lys	Trp	Leu	Pro	Leu
		115					120					125			
Tyr	Gly	Cys	Tyr	Phe	Ala	Gln	His	Gly	Gly	Ile	Tyr	Val	Lys	Arg	Ser
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Asp	Ala	Gly	Thr	Pro	Met	Tyr	Leu	Val	Ile	Phe	Pro	Glu	Gly	Thr	Arg
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Tyr	Asn	Pro	Glu	Gln	Thr	Lys	Val	Leu	Ser	Ala	Ser	Gln	Ala	Phe	Ala
			180					185					190		
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		195					200					205			
Lys	Ala	Thr	His	Val	Ala	Phe	Asp	Cys	Met	Lys	Asn	Tyr	Leu	Asp	Ala
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Ile	Tyr	Asp	Val	Thr	Val	Val	Tyr	Glu	Gly	Lys	Asp	Asp	Gly	Gly	Gln
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			260					265					270		
Glu	Gln	Glu	His	Met	Arg	Arg	Trp	Leu	His	Glu	Arg	Phe	Glu	Ile	Lys
		275					280					285			
Asp	Lys	Met	Leu	Ile	Glu	Phe	Tyr	Glu	Ser	Pro	Asp	Pro	Glu	Arg	Arg
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<400> 28
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<222> 1..23
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<221> primer_bind
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<221> allele
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<223> base C ; T in SEQ ID23

<221> primer_bind
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<221> primer_bind
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<223> potential microsequencing oligo 4-77.mis1

<221> primer_bind
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<210> 34
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<223> potential microsequencing oligo 99-217.mis1

<221> primer_bind
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<400> 34
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<210> 35
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<222> 1..23

<223> potential microsequencing oligo 99-221.mis1

<221> primer_bind

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<221> primer_bind

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<400> 38

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<210> 39

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<213> Homo Sapiens

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<210> 44
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58 complement

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<221> primer_bind

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<222> 25..47

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Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp Gly Val Trp
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Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe Phe Phe Glu
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Asn Tyr Thr Gly Val Gln His Gly Gly Ile Tyr Val Lys Arg Ser Ala
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Lys Phe Asn Glu Lys Glu Met Arg Asn Lys Leu Gln Ser Tyr Val Asp
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Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu Ile Lys Asp
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Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile Lys Lys Thr
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Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly Met Leu Met
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Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp Gly Val Trp
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Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp
   25           30           35           40
gac cgg ctg tac tgc gtc tac cag agc atg gtg ctc ttc ttc ttc gag 198
Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe Phe Phe Glu
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Asn Tyr Thr Gly Val Gln Met Tyr Leu Val Ile Phe Pro Glu Gly Thr
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agg tat aat cca gag caa aca aaa gtc ctt tca gct agt cag gca ttt 294
Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala Ser Gln Ala Phe
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gct gcc caa cgt ggc ctt gca gta tta aaa cat gtg cta aca cca cga 342
Ala Ala Gln Arg Gly Leu Ala Val Leu Lys His Val Leu Thr Pro Arg
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Ile Lys Ala Thr His Val Ala Phe Asp Cys Met Lys Asn Tyr Leu Asp
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Gln Arg Arg Glu Ser Pro Thr Met Thr Glu Phe Leu Cys Lys Glu Cys	
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cca aaa att cat att cac att gat cgt atc gac aaa aaa gat gtc cca	534
Pro Lys Ile His Ile His Ile Asp Arg Ile Asp Lys Lys Asp Val Pro	
155 160 165	
gaa gaa caa gaa cat atg aga aga tgg ctg cat gaa cgt ttc gaa atc	582
Glu Glu Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu Ile	
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Lys Asp Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro Asp Pro Glu Arg	
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Arg Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile Lys	
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Lys Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly Met	
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Leu Met Thr Asp Ala Gly Arg Lys Leu Tyr Val Asn Thr Trp Ile Tyr	
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Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp Gly Val Trp
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Asn Tyr Thr Gly Val Gln Ile Leu Leu Tyr Gly Asp Leu Pro Lys Asn
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Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp
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<400> 124

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Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp Gly Val Trp
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Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp
    25           30           35           40
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Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe Phe Phe Glu
    45           50           55
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Asn Tyr Thr Gly Val Gln Ile Leu Leu Tyr Gly Asp Leu Pro Lys Asn
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Lys Glu Asn Ile Ile Tyr Leu Ala Asn His Gln Ser Thr Val Asp Trp
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Ile Val Ala Asp Ile Leu Ala Ile Arg Gln Asn Ala Leu Gly His Val
    90           95           100
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Arg Tyr Val Leu Lys Glu Gly Leu Lys Trp Leu Pro Leu Tyr Gly Cys
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tac ttt gct cag cat gga gga atc tat gta aag cgc agt gcc aaa ttt      438
Tyr Phe Ala Gln His Gly Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe
    125          130          135
aac gag aaa gag atg cga aac aag ttg cag agc tac gtg gac gca gga      486
Asn Glu Lys Glu Met Arg Asn Lys Leu Gln Ser Tyr Val Asp Ala Gly
    140          145          150
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Thr Pro Met Tyr Leu Val Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro
    155          160          165
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Glu Gln Thr Lys Val Leu Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg
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<210> 125

<211> 77

<212> PRT

<213> Homo sapiens

<400> 125

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Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
1          5          10          15
Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
          20          25          30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
          35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Leu Thr
          50          55          60
Gly Leu Leu Leu Thr Ser Trp Pro Ser Gly Arg Met Arg
65          70          75

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<210> 126

<211> 238

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> 98..103

<223> Box II

<400> 126

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Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
1          5          10          15
Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
          20          25          30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
          35          40          45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln His Gly
          50          55          60
Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg
65          70          75          80
Asn Lys Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val
          85          90          95
Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu
          100          105          110
Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg Glu Phe Leu Cys Lys Glu
          115          120          125
Cys Pro Lys Ile His Ile His Ile Asp Arg Ile Asp Lys Lys Asp Val
          130          135          140
Pro Glu Glu Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu
145          150          155          160
Ile Lys Asp Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro Asp Pro Glu
          165          170          175

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Arg Arg Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile
      180      185      190
Lys Lys Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly
      195      200      205
Met Leu Met Thr Asp Ala Gly Arg Lys Leu Tyr Val Asn Thr Trp Ile
      210      215      220
Tyr Gly Thr Leu Leu Gly Cys Leu Trp Val Thr Ile Lys Ala
      225      230      235

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<210> 127
<211> 291
<212> PRT
<213> Homo sapiens

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<220>
<221> SITE
<222> 98..103
<223> Box II

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<221> SITE
<222> 149..157
<223> Box III

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<400> 127
Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
1      5      10      15
Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
      20      25      30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
      35      40      45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln His Gly
      50      55      60
Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg
65      70      75      80
Asn Lys Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val
      85      90      95
Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu
      100     105     110
Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg Gly Leu Ala Val Leu Lys
      115     120     125
His Val Leu Thr Pro Arg Ile Lys Ala Thr His Val Ala Phe Asp Cys
      130     135     140
Met Lys Asn Tyr Leu Asp Ala Ile Tyr Asp Val Thr Val Val Tyr Glu
145     150     155     160
Gly Lys Asp Asp Gly Gly Gln Arg Arg Glu Ser Pro Thr Met Thr Glu
      165     170     175
Phe Leu Cys Lys Glu Cys Pro Lys Ile His Ile His Ile Asp Arg Ile
      180     185     190
Asp Lys Lys Asp Val Pro Glu Glu Gln Glu His Met Arg Arg Trp Leu
      195     200     205
His Glu Arg Phe Glu Ile Lys Asp Lys Met Leu Ile Glu Phe Tyr Glu
      210     215     220
Ser Pro Asp Pro Glu Arg Arg Lys Arg Phe Pro Gly Lys Ser Val Asn
225     230     235     240
Ser Lys Leu Ser Ile Lys Lys Thr Leu Pro Ser Met Leu Ile Leu Ser
      245     250     255

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Gly Leu Thr Ala Gly Met Leu Met Thr Asp Ala Gly Arg Lys Leu Tyr
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 Val Asn Thr Trp Ile Tyr Gly Thr Leu Leu Gly Cys Leu Trp Val Thr
 275 280 285
 Ile Lys Ala
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<210> 128
 <211> 261
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
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 <223> Box II

<221> SITE
 <222> 119..127
 <223> Box III

<400> 128
 Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
 1 5 10 15
 Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
 20 25 30
 Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
 35 40 45
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Met Tyr
 50 55 60
 Leu Val Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys
 65 70 75 80
 Val Leu Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg Gly Leu Ala Val
 85 90 95
 Leu Lys His Val Leu Thr Pro Arg Ile Lys Ala Thr His Val Ala Phe
 100 105 110
 Asp Cys Met Lys Asn Tyr Leu Asp Ala Ile Tyr Asp Val Thr Val Val
 115 120 125
 Tyr Glu Gly Lys Asp Asp Gly Gly Gln Arg Arg Glu Ser Pro Thr Met
 130 135 140
 Thr Glu Phe Leu Cys Lys Glu Cys Pro Lys Ile His Ile His Ile Asp
 145 150 155 160
 Arg Ile Asp Lys Lys Asp Val Pro Glu Glu Gln Glu His Met Arg Arg
 165 170 175
 Trp Leu His Glu Arg Phe Glu Ile Lys Asp Lys Met Leu Ile Glu Phe
 180 185 190
 Tyr Glu Ser Pro Asp Pro Glu Arg Arg Lys Arg Phe Pro Gly Lys Ser
 195 200 205
 Val Asn Ser Lys Leu Ser Ile Lys Lys Thr Leu Pro Ser Met Leu Ile
 210 215 220
 Leu Ser Gly Leu Thr Ala Gly Met Leu Met Thr Asp Ala Gly Arg Lys
 225 230 235 240
 Leu Tyr Val Asn Thr Trp Ile Tyr Gly Thr Leu Leu Gly Cys Leu Trp
 245 250 255
 Val Thr Ile Lys Ala
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<210> 129

<211> 90

<212> PRT

<213> Homo sapiens

<400> 129

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Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
1           5           10           15
Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
          20           25           30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
          35           40           45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Asn Phe
          50           55           60
Ser Ala Lys Asn Val Gln Lys Phe Ile Phe Thr Leu Ile Val Ser Thr
65           70           75           80
Lys Lys Met Ser Gln Lys Asn Lys Asn Ile
          85           90

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<210> 130

<211> 68

<212> PRT

<213> Homo sapiens

<400> 130

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Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
1           5           10           15
Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
          20           25           30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
          35           40           45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Asp Ala
          50           55           60
Tyr Arg Ile Leu
65

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<210> 131

<211> 66

<212> PRT

<213> Homo sapiens

<400> 131

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Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
1           5           10           15
Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
          20           25           30
Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
          35           40           45
Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Arg Leu
          50           55           60
Asp Ser
65

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<210> 132

<211> 97

<212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> 81..83
 <223> Box I

<400> 132
 Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
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 Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
 20 25 30
 Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
 35 40 45
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
 50 55 60
 Leu Tyr Gly Asp Leu Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala
 65 70 75 80
 Asn His Gln Ser Thr Asp Val Ser Cys Asp Phe Ser Arg Arg Tyr Lys
 85 90 95
 Val

<210> 133
 <211> 182
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> 81..83
 <223> Box I

<400> 133
 Met Arg Tyr Leu Leu Pro Ser Val Val Leu Leu Gly Thr Ala Pro Thr
 1 5 10 15
 Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
 20 25 30
 Ala Arg Phe Tyr Gln Ala Leu Asp Asp Arg Leu Tyr Cys Val Tyr Gln
 35 40 45
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
 50 55 60
 Leu Tyr Gly Asp Leu Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala
 65 70 75 80
 Asn His Gln Ser Thr Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile
 85 90 95
 Arg Gln Asn Ala Leu Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu
 100 105 110
 Lys Trp Leu Pro Leu Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile
 115 120 125
 Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys
 130 135 140
 Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Asn Phe Ser Ala Lys Asn
 145 150 155 160
 Val Gln Lys Phe Ile Phe Thr Leu Ile Val Ser Thr Lys Lys Met Ser
 165 170 175

Gln Lys Asn Lys Asn Ile
180

<210> 134

<211> 315

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> 81..83

<223> Box I

<221> SITE

<222> 160..165

<223> Box II

<400> 134

Met	Arg	Tyr	Leu	Leu	Pro	Ser	Val	Val	Leu	Leu	Gly	Thr	Ala	Pro	Thr
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Tyr	Val	Leu	Ala	Trp	Gly	Val	Trp	Arg	Leu	Leu	Ser	Ala	Phe	Leu	Pro
		20						25					30		
Ala	Arg	Phe	Tyr	Gln	Ala	Leu	Asp	Arg	Leu	Tyr	Cys	Val	Tyr	Gln	
		35					40				45				
Ser	Met	Val	Leu	Phe	Phe	Phe	Glu	Asn	Tyr	Thr	Gly	Val	Gln	Ile	Leu
	50					55					60				
Leu	Tyr	Gly	Asp	Leu	Pro	Lys	Asn	Lys	Glu	Asn	Ile	Ile	Tyr	Leu	Ala
65					70				75						80
Asn	His	Gln	Ser	Thr	Val	Asp	Trp	Ile	Val	Ala	Asp	Ile	Leu	Ala	Ile
				85					90					95	
Arg	Gln	Asn	Ala	Leu	Gly	His	Val	Arg	Tyr	Val	Leu	Lys	Glu	Gly	Leu
			100					105					110		
Lys	Trp	Leu	Pro	Leu	Tyr	Gly	Cys	Tyr	Phe	Ala	Gln	His	Gly	Gly	Ile
		115				120					125				
Tyr	Val	Lys	Arg	Ser	Ala	Lys	Phe	Asn	Glu	Lys	Glu	Met	Arg	Asn	Lys
	130					135					140				
Leu	Gln	Ser	Tyr	Val	Asp	Ala	Gly	Thr	Pro	Met	Tyr	Leu	Val	Ile	Phe
145					150					155					160
Pro	Glu	Gly	Thr	Arg	Tyr	Asn	Pro	Glu	Gln	Thr	Lys	Val	Leu	Ser	Ala
				165					170					175	
Ser	Gln	Ala	Phe	Ala	Ala	Gln	Arg	Gly	Lys	Asp	Asp	Gly	Gly	Gln	Arg
			180					185					190		
Arg	Glu	Ser	Pro	Thr	Met	Thr	Glu	Phe	Leu	Cys	Lys	Glu	Cys	Pro	Lys
		195					200					205			
Ile	His	Ile	His	Ile	Asp	Arg	Ile	Asp	Lys	Lys	Asp	Val	Pro	Glu	Glu
	210					215					220				
Gln	Glu	His	Met	Arg	Arg	Trp	Leu	His	Glu	Arg	Phe	Glu	Ile	Lys	Asp
225					230					235					240
Lys	Met	Leu	Ile	Glu	Phe	Tyr	Glu	Ser	Pro	Asp	Pro	Glu	Arg	Arg	Lys
				245					250					255	
Arg	Phe	Pro	Gly	Lys	Ser	Val	Asn	Ser	Lys	Leu	Ser	Ile	Lys	Lys	Thr
			260					265					270		
Leu	Pro	Ser	Met	Leu	Ile	Leu	Ser	Gly	Leu	Thr	Ala	Gly	Met	Leu	Met
		275					280					285			
Thr	Asp	Ala	Gly	Arg	Lys	Leu	Tyr	Val	Asn	Thr	Trp	Ile	Tyr	Gly	Thr
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Leu Leu Gly Cys Leu Trp Val Thr Ile Lys Ala
 305 310 315

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 35 40 45
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
 50 55 60
 Leu Tyr Gly Asp Leu Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala
 65 70 75 80
 Asn His Gln Ser Thr Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile
 85 90 95
 Arg Gln Asn Ala Leu Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu
 100 105 110
 Lys Trp Leu Pro Leu Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile
 115 120 125
 Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys
 130 135 140
 Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val Ile Phe
 145 150 155 160
 Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala
 165 170 175
 Ser Gln Ala Phe Ala Ala Gln Arg Glu Phe Leu Cys Lys Glu Cys Pro
 180 185 190
 Lys Ile His Ile His Ile Asp Arg Ile Asp Lys Lys Asp Val Pro Glu
 195 200 205
 Glu Gln Glu His Met Arg Arg Trp Leu His Glu Arg Phe Glu Ile Lys
 210 215 220
 Asp Lys Met Leu Ile Glu Phe Tyr Glu Ser Pro Asp Pro Glu Arg Arg
 225 230 235 240
 Lys Arg Phe Pro Gly Lys Ser Val Asn Ser Lys Leu Ser Ile Lys Lys
 245 250 255
 Thr Leu Pro Ser Met Leu Ile Leu Ser Gly Leu Thr Ala Gly Met Leu
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 Met Thr Asp Ala Gly Arg Lys Leu Tyr Val Asn Thr Trp Ile Tyr Gly
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 Tyr Val Leu Ala Trp Gly Val Trp Arg Leu Leu Ser Ala Phe Leu Pro
 20 25 30
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 35 40 45
 Ser Met Val Leu Phe Phe Phe Glu Asn Tyr Thr Gly Val Gln Ile Leu
 50 55 60
 Leu Tyr Gly Asp Leu Pro Lys Asn Lys Glu Asn Ile Ile Tyr Leu Ala
 65 70 75 80
 Asn His Gln Ser Thr Val Asp Trp Ile Val Ala Asp Ile Leu Ala Ile
 85 90 95
 Arg Gln Asn Ala Leu Gly His Val Arg Tyr Val Leu Lys Glu Gly Leu
 100 105 110
 Lys Trp Leu Pro Leu Tyr Gly Cys Tyr Phe Ala Gln His Gly Gly Ile
 115 120 125
 Tyr Val Lys Arg Ser Ala Lys Phe Asn Glu Lys Glu Met Arg Asn Lys
 130 135 140
 Leu Gln Ser Tyr Val Asp Ala Gly Thr Pro Met Tyr Leu Val Ile Phe
 145 150 155 160
 Pro Glu Gly Thr Arg Tyr Asn Pro Glu Gln Thr Lys Val Leu Ser Ala
 165 170 175
 Ser Gln Ala Phe Ala Ala Gln Arg Gly
 180 185

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Phe	Phe	Phe	Glu	Asn	Tyr	Thr	Gly	Val	Gln	Ile	Leu	Leu	Tyr	Gly	Asp		
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Cys Pro Lys Leu His Ile His Phe Asp Arg Ile Asp Arg Asn Glu Val			
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cca gag gaa caa gaa cac atg aaa aag tgg ctt cat gag cgc ttt gag			872
Pro Glu Glu Gln Glu His Met Lys Lys Trp Leu His Glu Arg Phe Glu			
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ata aaa gat agg ttg ctc ata gag ttc tat gat tca cca gat cca gaa			920
Ile Lys Asp Arg Leu Leu Ile Glu Phe Tyr Asp Ser Pro Asp Pro Glu			
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Arg Arg Asn Lys Phe Pro Gly Lys Ser Val His Ser Arg Leu Ser Val			
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aag aag act tta cct tca gtg ttg atc ttg ggg agt ttg act gcg gtc			1016
Lys Lys Thr Leu Pro Ser Val Leu Ile Leu Gly Ser Leu Thr Ala Val			
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<222> 25..47

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<221> primer_bind

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<221> primer_bind
<222> 25..47
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<400> 240

aaaaaaaaatc aaattattgt accaaattcc ctaatatcag atgtgta

47

<210> 241

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<223> polymorphic fragment 99-1479-158

<221> allele

<222> 24

<223> polymorphic base C

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-1479-158.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1479-158.mis2

<400> 241

tttaaaaatc cacttgtaat cgccgctaatt tggagtgtat attcagg

47

<210> 242

<211> 47

<212> DNA

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<221> allele

<222> 24

<223> polymorphic base A

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-1479-379.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1479-379.mis2

<400> 242

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47

<210> 243

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<212> DNA
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<221> allele
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<223> potential microsequencing oligo 99-148-129.mis1

<221> primer_bind
<222> 25..47
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<221> allele
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-132.mis1

<221> primer_bind
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47

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<221> allele
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-139.mis1

<221> primer_bind
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<400> 245
tacaaataat tttgaattta atacataggg ctgcaaaaca aggttga 47

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<221> allele
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<223> polymorphic base A

<221> primer_bind
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<223> potential microsequencing oligo 99-148-140.mis1

<221> primer_bind
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<400> 246
acaaataatt ttgaatttaa tacatagggc tgcaaaacaa gggttgat 47

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<221> allele
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<223> polymorphic base A

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-148-182.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-148-182.mis2

<400> 247

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<210> 248

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<221> allele

<222> 24

<223> polymorphic base G

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-148-366.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-148-366.mis2

<400> 248

tccttgtaa aggtctctcc ctggtgctca cggctgccgc ctcaaag

47

<210> 249

<211> 47

<212> DNA

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<221> allele

<222> 24

<223> polymorphic base C

<221> primer_bind

<222> 1..23

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<221> primer_bind
<222> 25..47
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<400> 249
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47

<210> 250
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<223> polymorphic base G

<221> primer_bind
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<221> primer_bind
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<400> 250
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47

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<221> allele
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<223> potential microsequencing oligo 99-1481-285.mis1

<221> primer_bind
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<400> 251
tcccataacc tggttttgctt ctcgctctaa cctcaagatg gtataaa 47

<210> 252
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<221> allele
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<223> potential microsequencing oligo 99-1484-101.mis1

<221> primer_bind
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<400> 252
aaaaagatca aatataagca tgtaactcct ctccttaaaa tctcagt 47

<210> 253
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<222> 1..47
<223> polymorphic fragment 99-1484-328

<221> allele
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<223> polymorphic base G

<221> primer_bind
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<223> potential microsequencing oligo 99-1484-328.mis1

<221> primer_bind
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<400> 253
ggacacgtgg tcatgaggag tttgaaggga ttcagttttc agatccc 47

<210> 254

<211> 47
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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-1485-251.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 99-1485-251.mis2

<400> 254
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47

<210> 255
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<223> polymorphic fragment 99-1490-381

<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-1490-381.mis1

<221> primer_bind
<222> 25..47
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<400> 255
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47

<210> 256
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<223> polymorphic fragment 99-1493-280

<221> allele
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<223> polymorphic base A

<221> primer_bind
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<223> potential microsequencing oligo 99-1493-280.mis1

<221> primer_bind
<222> 25..47
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<400> 256
ggatgacaga gtattgttgg aggaatgggg tttggctgct tgttttt

47

<210> 257
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<223> polymorphic fragment 99-151-94

<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-151-94.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 99-151-94.mis2

<400> 257
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47

<210> 258
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<223> polymorphic fragment 99-211-291

<221> allele

<222> 24
<223> polymorphic base A

<221> primer_bind
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<223> potential microsequencing oligo 99-211-291.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-211-291.mis2

<400> 258
ctggttatat cagactgacc ttcatgtttt caacagggtca atgcctt

47

<210> 259
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<220>
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<223> polymorphic fragment 99-213-37

<221> allele
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<223> polymorphic base T

<221> primer_bind
<222> 1..22
<223> potential microsequencing oligo 99-213-37.mis1

<221> primer_bind
<222> 24..45
<223> complement potential microsequencing oligo 99-213-37.mis2

<400> 259
gtgcttccgg ctgcaggact gttggaggac tccagtgtct gacag

45

<210> 260
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<223> polymorphic fragment 99-221-442

<221> allele
<222> 24
<223> polymorphic base A

<221> primer_bind
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<223> potential microsequencing oligo 99-221-442.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-221-442.mis2

<400> 260

tgcctttgta gatatgcatg ggaattccat gacctagcca gacgaat

47

<210> 261

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 99-222-109

<221> allele

<222> 24

<223> polymorphic base C

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-222-109.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-222-109.mis2

<400> 261

caggtgagga gtgctggatt ggccacgata tgaatttctt cagcagt

47

<210> 262

<211> 47

<212> DNA

<213> Homo Sapiens

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<222> 1..47

<223> polymorphic fragment 4-14-107, variant version of SEQ ID185

<221> allele

<222> 24

<223> base G ; A in SEQ ID185

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-14-107.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-14-107.mis2

<400> 262
ctaaacaacc accaaatgca tacggcaacc aggcaaatgc ctgatag 47

<210> 263
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<223> polymorphic fragment 4-14-317, variant version of SEQ ID186

<221> allele
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-14-317.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 4-14-317.mis2

<400> 263
cataacatgc aaggtgggca agagaaagag gtgggcacag ctcatga 47

<210> 264
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<212> DNA
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<223> polymorphic fragment 4-14-35, variant version of SEQ ID187

<221> allele
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<223> base T ; C in SEQ ID187

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-14-35.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-14-35.mis2

<400> 264
atccaacaca gaaaccgcta aaatcaggca gaagctgtct gcagaga 47

<210> 265
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<221> allele
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<223> base T ; C in SEQ ID188

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-20-149.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-20-149.mis2

<400> 265
tttttgctgt gtcttcaaag tgattcttgg tttattgcct gctaagg

47

<210> 266
<211> 47
<212> DNA
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<221> allele
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<223> base T ; A in SEQ ID189

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-20-77.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-20-77.mis2

<400> 266
tgcaacatga agattctgaa gggctcttgt tgtctgagaa cacatct

47

<210> 267
<211> 47
<212> DNA
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<223> polymorphic fragment 4-22-174, variant version of SEQ ID190

<221> allele
<222> 24
<223> base C ; A in SEQ ID190

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-22-174.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-22-174.mis2

<400> 267
ggattgtgca gaagttgcct ttcctgttca aaaatgttaa tttgttt

47

<210> 268
<211> 47
<212> DNA
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<223> polymorphic fragment 4-22-176, variant version of SEQ ID191

<221> allele
<222> 24
<223> base G ; A in SEQ ID191

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-22-176.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-22-176.mis2

<400> 268
attgtgcaga agttgccttt catgttcaaa aatgttaatt tgtttgt

47

<210> 269
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<223> polymorphic fragment 4-26-60, variant version of SEQ ID192

<221> allele
<222> 24
<223> base G ; A in SEQ ID192

<221> primer_bind
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<223> potential microsequencing oligo 4-26-60.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-26-60.mis2

<400> 269
gatgggaaag tgcattcttaa gacgggtagc aggccaagga gcgactt

47

<210> 270
<211> 47
<212> DNA
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<220>
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<223> polymorphic fragment 4-26-72, variant version of SEQ ID193

<221> allele
<222> 24
<223> base G ; A in SEQ ID193

<221> primer_bind
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<223> potential microsequencing oligo 4-26-72.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-26-72.mis2

<400> 270
catcttaaga cagtttagcag gccgaggagc gactttaag ggtgagc

47

<210> 271
<211> 47
<212> DNA
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<220>
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<223> polymorphic fragment 4-3-130, variant version of SEQ ID194

<221> allele
<222> 24
<223> base G ; A in SEQ ID194

<221> primer_bind

<222> 1..23
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<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-3-130.mis2

<400> 271
tattgggcct aaaacagtat tctgtaaagc ttaaattggt attaact 47

<210> 272
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<212> DNA
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<220>
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<223> polymorphic fragment 4-38-63, variant version of SEQ ID195

<221> allele
<222> 24
<223> base G ; A in SEQ ID195

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-38-63.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-38-63.mis2

<400> 272
tataagttat aagaaaaatca ggcggaggct aaactttttt tttgttt 47

<210> 273
<211> 47
<212> DNA
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<220>
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<222> 1..47
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<221> allele
<222> 24
<223> base T ; G in SEQ ID196

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-38-83.mis1

<221> primer_bind
<222> 25..47

<223> complement potential microsequencing oligo 4-38-83.mis2

<400> 273

ggcagaggct aaactttttt tttttttggc aatgctgttg agaatat

47

<210> 274

<211> 47

<212> DNA

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<220>

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<222> 1..47

<223> polymorphic fragment 4-4-152, variant version of SEQ ID197

<221> allele

<222> 24

<223> base T ; C in SEQ ID197

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-4-152.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-4-152.mis2

<400> 274

tactttccca ttgttcctga ctttggtatc ctatatataa acagaaa

47

<210> 275

<211> 47

<212> DNA

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<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 4-4-187, variant version of SEQ ID198

<221> allele

<222> 24

<223> base T ; A in SEQ ID198

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-4-187.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-4-187.mis2

<400> 275

tataaacaga aacatggatg agttaaaaaa aaaaaaaaaa aaaaaaa

47

<210> 276
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<212> DNA
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<221> allele
<222> 24
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<221> primer_bind
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<223> potential microsequencing oligo 4-4-288.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-4-288.mis2

<400> 276
ctgtcatcaa ctaattttca caactaccta tggttttgatt tcatgta

47

<210> 277
<211> 47
<212> DNA
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<220>
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<221> allele
<222> 24
<223> base T ; C in SEQ ID200

<221> primer_bind
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<223> potential microsequencing oligo 4-42-304.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-42-304.mis2

<400> 277
attattttaa actattttatg taatcttatt ttcaggggtt tttaatt

47

<210> 278
<211> 47
<212> DNA
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<220>
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<223> polymorphic fragment 4-42-401, variant version of SEQ ID201

<221> allele
<222> 24
<223> base C ; A in SEQ ID201

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-42-401.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-42-401.mis2

<400> 278
taagaaagaa ttctgtgttc tggccaaagt ttaaaccac agagcca

47

<210> 279
<211> 47
<212> DNA
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<220>
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<223> polymorphic fragment 4-43-328, variant version of SEQ ID202

<221> allele
<222> 24
<223> base T ; C in SEQ ID202

<221> primer_bind
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<223> potential microsequencing oligo 4-43-328.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-43-328.mis2

<400> 279
agaattctgt gttctggcca aagtttaaac ccacagagcc agtttaa

47

<210> 280
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<220>
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<223> polymorphic fragment 4-43-70, variant version of SEQ ID203

<221> allele
<222> 24
<223> base C ; G in SEQ ID203

<221> primer_bind
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<223> potential microsequencing oligo 4-43-70.mis1

<221> primer_bind
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<400> 280
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47

<210> 281
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<220>
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<221> allele
<222> 24
<223> base T ; C in SEQ ID204

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-50-209.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-50-209.mis2

<400> 281
atatagagtg tgcattccctg acattgaaac tgaaggcttt atgggtt

47

<210> 282
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<221> allele
<222> 24
<223> base T ; G in SEQ ID205

<221> primer_bind
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<223> potential microsequencing oligo 4-50-293.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 4-50-293.mis2

<400> 282
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<210> 283
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<221> allele
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-50-323.mis1

<221> primer_bind
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<400> 283
tttaaaacat tgatgaatct ttattactac aaaagggttc gatttag 47

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<221> allele
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<221> primer_bind
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<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-50-329.mis2

<400> 284

acattgatga atctttatta ctataaaagg gttcgattta ggctagc

47

<210> 285

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<221> allele

<222> 24

<223> base T ; A in SEQ ID208

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-50-330.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-50-330.mis2

<400> 285

cattgatgaa tctttattac tactaaaggg ttcgatttag gctagcc

47

<210> 286

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<221> allele

<222> 24

<223> base C ; A in SEQ ID209

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-52-163.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-52-163.mis2

<400> 286

gaacaggata ttcttaacta ccacagaatt ttacacatct attgttt

47

<210> 287
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<221> primer_bind
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<221> primer_bind
<222> 25..47
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<400> 287
tccatgtcat tattattcaa aagtttaaaa aatacacaag gtgaaaa

47

<210> 288
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<212> DNA
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<221> allele
<222> 24
<223> base G ; A in SEQ ID211

<221> primer_bind
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<223> potential microsequencing oligo 4-53-258.mis1

<221> primer_bind
<222> 25..47
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gagaaatcat gcagagagaa tgcgttctca ctcaaatttt aacctaa

47

<210> 289
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<221> allele

<222> 24

<223> base T ; A in SEQ ID212

<221> primer_bind

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<223> potential microsequencing oligo 4-54-283.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-54-283.mis2

<400> 289

aagtagtttt tcacactttc tctttgatac aatcgatggc ttaatct

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<210> 290

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<212> DNA

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<222> 1..47

<223> polymorphic fragment 4-54-388, variant version of SEQ ID213

<221> allele

<222> 24

<223> base C ; A in SEQ ID213

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-54-388.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-54-388.mis2

<400> 290

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47

<210> 291

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<221> allele

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<223> base T ; A in SEQ ID214

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-55-70.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-55-70.mis2

<400> 291

tattaagaac ctaggtttta aaatactctc tatcgatac atcttta

47

<210> 292

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<223> polymorphic fragment 4-55-95, variant version of SEQ ID215

<221> allele

<222> 24

<223> base C ; A in SEQ ID215

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-55-95.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-55-95.mis2

<400> 292

ctctctatcg tatacatctt tacccacgct gcagcgcaa gactcca

47

<210> 293

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<223> polymorphic fragment 4-56-159, variant version of SEQ ID216

<221> allele

<222> 24

<223> base T ; C in SEQ ID216

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-56-159.mis1

<221> primer_bind
<222> 25..47
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<400> 293
aagttttcct tctcttctgt agatgtctcc atgttacagt caactat

47

<210> 294
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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 4-56-213.mis1

<221> primer_bind
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<400> 294
atggctcatg ttcactctgg ttcgccttca gaggagtttg atattttt

47

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<223> polymorphic fragment 4-58-289, variant version of SEQ ID218

<221> allele
<222> 24
<223> base C ; G in SEQ ID218

<221> primer_bind
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<223> potential microsequencing oligo 4-58-289.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 4-58-289.mis2

<400> 295
catacctgca gcctgctttt ggtcaggggt gactacttta cctgcaa

47

<210> 296
<211> 47
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<220>
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<221> allele
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<223> base C ; A in SEQ ID219

<221> primer_bind
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<223> potential microsequencing oligo 4-58-318.mis1

<221> primer_bind
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<400> 296
tgactacttt acctgcaata tttctttgca agtttatctt ctccttt

47

<210> 297
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<223> polymorphic fragment 4-60-266, variant version of SEQ ID220

<221> allele
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<223> base T ; G in SEQ ID220

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-60-266.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 4-60-266.mis2

<400> 297

aacaggacca agacactgca ttatataaaag tttcagtatt tcttagc

47

<210> 298

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

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<222> 1..47

<223> polymorphic fragment 4-60-293, variant version of SEQ ID221

<221> allele

<222> 24

<223> base T ; C in SEQ ID221

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-60-293.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-60-293.mis2

<400> 298

aagtttcagt atttcttagc agatgaagcc agcaggaagt cctccta

47

<210> 299

<211> 47

<212> DNA

<213> Homo Sapiens

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<222> 1..47

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<221> allele

<222> 24

<223> base T ; G in SEQ ID222

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-84-241.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-84-241.mis2

<400> 299

gaaaaaaaaa tagtgactgc cactgtgaat aattcagttc ttcagaa

47

<210> 300

<211> 47

<212> DNA
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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 4-84-262.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 4-84-262.mis2

<400> 300
acggtgaata attcagttct tcagaagcag caacatgata tcatgga 47

<210> 301
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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 4-86-206.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-86-206.mis2

<400> 301
gtattcaaata caggacacac cacgaatggc atctacacgt taacatt 47

<210> 302
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<222> 1..47
<223> polymorphic fragment 4-86-309, variant version of SEQ ID225

<221> allele
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<223> base T ; A in SEQ ID225

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-86-309.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 4-86-309.mis2

<400> 302
tggctctagg caggccactt tagtgagtga ggaaccagag agcagaa

47

<210> 303
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<221> allele
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 4-88-349.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 4-88-349.mis2

<400> 303
gaaactaaaa gacaatattc agtctgagat tttccaagtt ctttatg

47

<210> 304
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<212> DNA
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<220>
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<223> polymorphic fragment 4-89-87, variant version of SEQ ID227

<221> allele
<222> 24

<223> base T ; C in SEQ ID227

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 4-89-87.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 4-89-87.mis2

<400> 304

ttcttccctg aacgctggtt tcatatagtt tttgtgttga gaataga

47

<210> 305

<211> 47

<212> DNA

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<220>

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<222> 1..47

<223> polymorphic fragment 99-123-184, variant version of SEQ ID228

<221> allele

<222> 24

<223> base C ; G in SEQ ID228

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-123-184.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-123-184.mis2

<400> 305

ccagcccaga acattcacca gctcggccaa gagttctgct gggtttt

47

<210> 306

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<223> polymorphic fragment 99-128-202, variant version of SEQ ID229

<221> allele

<222> 24

<223> base C ; A in SEQ ID229

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-128-202.mis1

<221> primer_bind
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<400> 306
aatgtctgtt tcttagagaa ctgcaacaca cacacataca tacacac 47

<210> 307
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<220>
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<221> allele
<222> 24
<223> base G ; A in SEQ ID230

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-128-275.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-128-275.mis2

<400> 307
acaccctac ctcacatgtg taggcaaag tatgcatata tgtctct 47

<210> 308
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<220>
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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-128-313.mis1

<221> primer_bind
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<400> 308
tatgtctcta gacagatata catgagattc tatttggcat agaaaaa

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<210> 309
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<221> primer_bind
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<223> potential microsequencing oligo 99-128-60.mis1

<221> primer_bind
<222> 25..47
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<400> 309
gcactgtgac ccaggcgcta ggttctctctt acagtgcac tccgaca

47

<210> 310
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<223> polymorphic fragment 99-12907-295, variant version of SEQ ID233

<221> allele
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<221> primer_bind
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<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-12907-295.mis2

<400> 310
gctatatggc attatatctc cacggggcag acctgatgta caagatg

47

<210> 311

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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-130-58.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 99-130-58.mis2

<400> 311
aaagcaaaaag agcttcaaaa atatctcagg agtgtgcata tggcgag

47

<210> 312
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<223> polymorphic fragment 99-134-362, variant version of SEQ ID235

<221> allele
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-134-362.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 99-134-362.mis2

<400> 312
caaaacactc atggttagtta gattattatt cctattacaa agataag

47

<210> 313
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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-140-130.mis1

<221> primer_bind
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<223> complement potential microsequencing oligo 99-140-130.mis2

<400> 313
tggtcaaaag cagctacaga ccatatgtaa acaattgagc atggctg

47

<210> 314
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<221> allele
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<221> primer_bind
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<223> potential microsequencing oligo 99-1462-238.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1462-238.mis2

<400> 314
ccctttcaag gttagtaact catctgctgt gtttctgctt cagaagg

47

<210> 315
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<221> allele

<222> 24
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<221> primer_bind
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<223> potential microsequencing oligo 99-147-181.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-147-181.mis2

<400> 315
gtgtcatgaa aaagagcatg atagaaagaa aaacttaaata ctttata

47

<210> 316
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<223> polymorphic fragment 99-1474-156, variant version of SEQ ID239

<221> allele
<222> 24
<223> base T ; G in SEQ ID239

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1474-156.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1474-156.mis2

<400> 316
cttgtactca taagttaaata atttataaca agaagaaata tggactt

47

<210> 317
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<223> polymorphic fragment 99-1474-359, variant version of SEQ ID240

<221> allele
<222> 24
<223> base G ; A in SEQ ID240

<221> primer_bind
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<223> potential microsequencing oligo 99-1474-359.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1474-359.mis2

<400> 317

aaaaaaaatc aaattattgt accgaattcc ctaatatcag atgtgta

47

<210> 318

<211> 47

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<222> 1..47

<223> polymorphic fragment 99-1479-158, variant version of SEQ ID241

<221> allele

<222> 24

<223> base T ; C in SEQ ID241

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-1479-158.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1479-158.mis2

<400> 318

tttaaaaaatc cacttgtaat cgctgctaattcaggatgtat attcagg

47

<210> 319

<211> 47

<212> DNA

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<222> 1..47

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<221> allele

<222> 24

<223> base G ; A in SEQ ID242

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-1479-379.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1479-379.mis2

<400> 319
gtagagctgt gtactgaggt caggaagca gctcatggta cagcctt 47

<210> 320
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<220>
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<221> allele
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<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-129.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-129.mis2

<400> 320
ttcatatcta tacaaataat ttgaattta atacataggg ctgcaaa 47

<210> 321
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<212> DNA
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<220>
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<223> polymorphic fragment 99-148-132, variant version of SEQ ID244

<221> allele
<222> 24
<223> base T ; C in SEQ ID244

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-132.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-132.mis2

<400> 321
atatctatac aaataatttt gaatttaata catagggctg caaaaca 47

<210> 322
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<212> DNA
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<220>
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<223> polymorphic fragment 99-148-139, variant version of SEQ ID245

<221> allele
<222> 24
<223> base T ; C in SEQ ID245

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-139.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-139.mis2

<400> 322
tacaaataat tttgaattta atatataagg ctgcaaaaaca aggttga

47

<210> 323
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<220>
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<223> polymorphic fragment 99-148-140, variant version of SEQ ID246

<221> allele
<222> 24
<223> base G ; A in SEQ ID246

<221> primer_bind
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<223> potential microsequencing oligo 99-148-140.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-140.mis2

<400> 323
acaaataatt ttgaatttaa tacgtagggc tgcaaaaaca gggttgat

47

<210> 324
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-148-182, variant version of SEQ ID247

<221> allele
<222> 24
<223> base G ; A in SEQ ID247

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-182.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-182.mis2

<400> 324
ttgatgttga tatgggcaac tgtgtgttgg atggtcccaa agcattc

47

<210> 325
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-148-366, variant version of SEQ ID248

<221> allele
<222> 24
<223> base T ; G in SEQ ID248

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-366.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-366.mis2

<400> 325
tccttgtcaa aggtctctcc ctgttgctca cggctgccgc ctcaaag

47

<210> 326
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-148-76, variant version of SEQ ID249

<221> allele
<222> 24
<223> base T ; C in SEQ ID249

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-148-76.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-148-76.mis2

<400> 326
tgatagaatg ccttcctgaa ttattactct tgatggcttc ataaaac

47

<210> 327
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-1480-290, variant version of SEQ ID250

<221> allele
<222> 24
<223> base T ; G in SEQ ID250

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1480-290.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1480-290.mis2

<400> 327
tgcaccatct tcaccacaac ccctggcaac cactgacatct ttactg

47

<210> 328
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-1481-285, variant version of SEQ ID251

<221> allele
<222> 24
<223> base T ; G in SEQ ID251

<221> primer_bind

<222> 1..23
 <223> potential microsequencing oligo 99-1481-285.mis1

<221> primer_bind
 <222> 25..47
 <223> complement potential microsequencing oligo 99-1481-285.mis2

<400> 328
 tcccataacc tgttttgctt ctctctctaa cctcaagatg gtataaa

47

<210> 329
 <211> 47
 <212> DNA
 <213> Homo Sapiens

<220>
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 <222> 1..47
 <223> polymorphic fragment 99-1484-101, variant version of SEQ ID252

<221> allele
 <222> 24
 <223> base C ; A in SEQ ID252

<221> primer_bind
 <222> 1..23
 <223> potential microsequencing oligo 99-1484-101.mis1

<221> primer_bind
 <222> 25..47
 <223> complement potential microsequencing oligo 99-1484-101.mis2

<400> 329
 aaaaagatca aatataagca tgtcactcct ctccttaaaa tctcagt

47

<210> 330
 <211> 47
 <212> DNA
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<220>
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 <222> 1..47
 <223> polymorphic fragment 99-1484-328, variant version of SEQ ID253

<221> allele
 <222> 24
 <223> base C ; G in SEQ ID253

<221> primer_bind
 <222> 1..23
 <223> potential microsequencing oligo 99-1484-328.mis1

<221> primer_bind
 <222> 25..47

<223> complement potential microsequencing oligo 99-1484-328.mis2

<400> 330

ggacacgtgg tcatgaggag tttcaaggga ttcagttttc agatccc

47

<210> 331

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 99-1485-251, variant version of SEQ ID254

<221> allele

<222> 24

<223> base T ; G in SEQ ID254

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-1485-251.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1485-251.mis2

<400> 331

gattgccttg atatatgctc ccatagaacc aagaatgtcc ccttttc

47

<210> 332

<211> 47

<212> DNA

<213> Homo Sapiens

<220>

<221> allele

<222> 1..47

<223> polymorphic fragment 99-1490-381, variant version of SEQ ID255

<221> allele

<222> 24

<223> base T ; C in SEQ ID255

<221> primer_bind

<222> 1..23

<223> potential microsequencing oligo 99-1490-381.mis1

<221> primer_bind

<222> 25..47

<223> complement potential microsequencing oligo 99-1490-381.mis2

<400> 332

tgacacgtgg aaataccatg tcatggtacg ctactgtgca tctcttc

47

<210> 333
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..47
<223> polymorphic fragment 99-1493-280, variant version of SEQ ID256

<221> allele
<222> 24
<223> base G ; A in SEQ ID256

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-1493-280.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-1493-280.mis2

<400> 333
ggatgacaga gtattgttgg agggatgggg tttggctgct tgttttt

47

<210> 334
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-151-94, variant version of SEQ ID257

<221> allele
<222> 24
<223> base G ; A in SEQ ID257

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-151-94.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-151-94.mis2

<400> 334
attgagatca ttgataagga aatgttctaa aatttcaaaa tctatat

47

<210> 335
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-211-291, variant version of SEQ ID258

<221> allele
<222> 24
<223> base G ; A in SEQ ID258

<221> primer_bind
<222> 1..23
<223> potential microsequencing oligo 99-211-291.mis1

<221> primer_bind
<222> 25..47
<223> complement potential microsequencing oligo 99-211-291.mis2

<400> 335
ctggttatat cagactgacc ttcgtgtttt caacaggtca atgcctt

47

<210> 336
<211> 46
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..46
<223> polymorphic fragment 99-213-37, variant version of SEQ ID259

<221> allele
<222> 23
<223> base GC ; T in SEQ ID259

<221> primer_bind
<222> 1..22
<223> potential microsequencing oligo 99-213-37.mis1

<221> primer_bind
<222> 24..46
<223> complement potential microsequencing oligo 99-213-37.mis2

<400> 336
gtgcttccgg ctgcaggact gtgcggagga ctccagtgtc tgacag

46

<210> 337
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 1..47
<223> polymorphic fragment 99-221-442, variant version of SEQ ID260

<221> allele
 <222> 24
 <223> base C ; A in SEQ ID260

<221> primer_bind
 <222> 1..23
 <223> potential microsequencing oligo 99-221-442.mis1

<221> primer_bind
 <222> 25..47
 <223> complement potential microsequencing oligo 99-221-442.mis2

<400> 337
 tgcctttgta gatatgcatg ggacttccat gacctagcca gacgaat

47

<210> 338
 <211> 47
 <212> DNA
 <213> Homo Sapiens

<220>
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 <222> 1..47
 <223> polymorphic fragment 99-222-109, variant version of SEQ ID261

<221> allele
 <222> 24
 <223> base T ; C in SEQ ID261

<221> primer_bind
 <222> 1..23
 <223> potential microsequencing oligo 99-222-109.mis1

<221> primer_bind
 <222> 25..47
 <223> complement potential microsequencing oligo 99-222-109.mis2

<400> 338
 caggtgagga gtgctggatt ggctacgata tgaatttctt cagcagt

47

<210> 339
 <211> 18
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> misc_feature
 <222> 1..18
 <223> upstream amplification primer for SEQ 185, SEQ 262, SEQ 186, SEQ 263, SEQ 187, SEQ 264

<400> 339
 tctaacctct catccaac

18

<210> 340
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 188, SEQ 265, SEQ 189, SEQ 266

<400> 340
gttatcgtga gacttttttc 19

<210> 341
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 190, SEQ 267, SEQ 191, SEQ 268

<400> 341
tgctggtgct gtgataac 18

<210> 342
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 192, SEQ 269, SEQ 193, SEQ 270

<400> 342
tacagccctg taagacac 18

<210> 343
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 194, SEQ 271

<400> 343
cagtatgttc aatgcacag 19

<210> 344
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 195, SEQ 272, SEQ 196, SEQ 273

<400> 344
aaaacatcga catgggac 18

<210> 345
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 197, SEQ 274, SEQ 198, SEQ 275, SEQ 199, SEQ 276

<400> 345
agcatttcga gtcatgtg 18

<210> 346
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 200, SEQ 277, SEQ 201, SEQ 278

<400> 346
ccctctttcc tcatgtag 18

<210> 347
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 202, SEQ 279, SEQ 203, SEQ 280

<400> 347
taactcgtaa acagagaac 19

<210> 348
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 204, SEQ 281, SEQ 205, SEQ 282, SEQ 206, SEQ 283, SEQ 207, SEQ 284, SEQ 208, SEQ 285

<400> 348
gcgtattgaa gctctttg 18

<210> 349
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 209, SEQ 286, SEQ 210, SEQ 287

<400> 349
aacacgggga ttttaggc 18

<210> 350
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 211, SEQ 288

<400> 350
cacatactaa ggctaattg 19

<210> 351
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 212, SEQ 289, SEQ 213, SEQ 290

<400> 351
gttgctggaa cctatttg 18

<210> 352
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 214, SEQ 291, SEQ 215, SEQ 292

<400> 352
tcgatggctt aatctacc 18

<210> 353
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 216, SEQ 293, SEQ 217, SEQ 294

<400> 353
aaagaggagt aaatgggg 18

<210> 354
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 218, SEQ 295, SEQ 219, SEQ 296

<400> 354
tccccacagc taagagcc 18

<210> 355
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 220, SEQ 297, SEQ 221, SEQ 298

<400> 355
atacctaatt tcaggggg 18

<210> 356

<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 222, SEQ 299, SEQ 223, SEQ 300

<400> 356
ttaacagagt accttgag 19

<210> 357
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 224, SEQ 301, SEQ 225, SEQ 302

<400> 357
gtacagcctt ttgcttac 18

<210> 358
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 226, SEQ 303

<400> 358
aacgtgtcat agaaagcc 18

<210> 359
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 227, SEQ 304

<400> 359
gctgatgagt tagataacc 19

<210> 360
<211> 18

<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 228, SEQ 305

<400> 360
aaagccagga ctagaagg 18

<210> 361
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 229, SEQ 306, SEQ 230, SEQ 307, SEQ 231, SEQ 308, SEQ 232, SEQ 309

<400> 361
gaccagggtt taagttag 18

<210> 362
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 233, SEQ 310

<400> 362
tctgttagga cctgtgag 18

<210> 363
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 234, SEQ 311

<400> 363
ccataacagc tagtacaac 19

<210> 364
<211> 18

<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 235, SEQ 312

<400> 364
tggaaaggta ctcagaag 18

<210> 365
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 236, SEQ 313

<400> 365
agagcatagt ataaagcag 19

<210> 366
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 237, SEQ 314

<400> 366
ctagaagtag ctttaacag 19

<210> 367
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 238, SEQ 315

<400> 367
gcagccaatc ttatatatttc 19

<210> 368
<211> 19
<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..19

<223> upstream amplification primer for SEQ 239, SEQ 316, SEQ 240, SEQ 317

<400> 368

aaggttgtag agtagaaag

19

<210> 369

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 241, SEQ 318, SEQ 242, SEQ 319

<400> 369

caactgacac tataaccc

18

<210> 370

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 243, SEQ 320, SEQ 244, SEQ 321, SEQ 245, SEQ 322, SEQ 246, SEQ 323, SEQ 247, SEQ 324, SEQ 248, SEQ 325, SEQ 249, SEQ 326

<400> 370

cagtggagtg tttatgtg

18

<210> 371

<211> 19

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..19

<223> upstream amplification primer for SEQ 250, SEQ 327

<400> 371

ttgcacaaaa ggtatagag

19

<210> 372

<211> 19

<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 251, SEQ 328

<400> 372
aggctcccct tttgagttg 19

<210> 373
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> upstream amplification primer for SEQ 252, SEQ 329, SEQ 253, SEQ 330

<400> 373
atcctttcta gctgggag 18

<210> 374
<211> 20
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..20
<223> upstream amplification primer for SEQ 254, SEQ 331

<400> 374
gtttaagaat gtgtgatggg 20

<210> 375
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 255, SEQ 332

<400> 375
aaggcaacag cgttgtgac 19

<210> 376
<211> 18
<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 256, SEQ 333

<400> 376

ttttgggggt tttcagtg

18

<210> 377

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 257, SEQ 334

<400> 377

aacacaacag caaatccc

18

<210> 378

<211> 18

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..18

<223> upstream amplification primer for SEQ 258, SEQ 335

<400> 378

tccttacttg taaccccc

18

<210> 379

<211> 20

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> 1..20

<223> upstream amplification primer for SEQ 259, SEQ 336

<400> 379

atactggcag cgtgtgcttc

20

<210> 380

<211> 19

<212> DNA

<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..19
<223> upstream amplification primer for SEQ 260, SEQ 337

<400> 380
ccctttttct tcactgttc 19

<210> 381
<211> 20
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..20
<223> upstream amplification primer for SEQ 261, SEQ 338

<400> 381
aggggagatg agggaagttg 20

<210> 382
<211> 20
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..20
<223> downstream amplification primer for SEQ 185, SEQ 262, SEQ 186, SEQ 263, SEQ 187, SEQ 264

<400> 382
gactgtatcc tttgatgcac 20

<210> 383
<211> 20
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..20
<223> downstream amplification primer for SEQ 188, SEQ 265, SEQ 189, SEQ 266

<400> 383
gcataattgt gcttgactgg 20

<210> 384
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> downstream amplification primer for SEQ 190, SEQ 267, SEQ 191, SEQ 268

<400> 384
tgctgagagg agcttttg 18

<210> 385
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> downstream amplification primer for SEQ 192, SEQ 269, SEQ 193, SEQ 270

<400> 385
tgaggactgc taggaaag 18

<210> 386
<211> 20
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..20
<223> downstream amplification primer for SEQ 194, SEQ 271

<400> 386
acaaaatcag gaacaatggg 20

<210> 387
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> downstream amplification primer for SEQ 195, SEQ 272, SEQ 196, SEQ 273

<400> 387
ttgcattttc cccccaac 18

<210> 388
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> downstream amplification primer for SEQ 197, SEQ 274, SEQ 198, SEQ 275, SEQ 199, SEQ 276

<400> 388
accatttgga caatgggg 18

<210> 389
<211> 20
<212> DNA
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<220>
<221> misc_feature
<222> 1..20
<223> downstream amplification primer for SEQ 200, SEQ 277, SEQ 201, SEQ 278

<400> 389
gctcttaaac tggctctgtg 20

<210> 390
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> downstream amplification primer for SEQ 202, SEQ 279, SEQ 203, SEQ 280

<400> 390
ggcatgactt cacgtttc 18

<210> 391
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> downstream amplification primer for SEQ 204, SEQ 281, SEQ 205, SEQ 282, SEQ 206, SEQ 283, SEQ 207, SEQ 284, SEQ 208, SEQ 285

<400> 391
aggatcttct acagtcac 18

<210> 392
<211> 20
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..20
<223> downstream amplification primer for SEQ 209, SEQ 286, SEQ 210, SEQ 287

<400> 392
tggtagcggtt tgaaatcatc 20

<210> 393
<211> 20
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..20
<223> downstream amplification primer for SEQ 211, SEQ 288

<400> 393
tataagcaca aataggttcc 20

<210> 394
<211> 18
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> 1..18
<223> downstream amplification primer for SEQ 212, SEQ 289, SEQ 213, SEQ 290

<400> 394
gaataactga ggggagtg 18

<210> 395
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<400> 395
gtgaatctcc ttttccaag 19

<210> 396
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<400> 396
ctaaggtggt gtagacag 18

<210> 397
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<400> 397
cacctcgata aatcaagtcc 20

<210> 398
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<223> downstream amplification primer for SEQ 220, SEQ 297, SEQ 221, SEQ 298

<400> 398
gttcacttaa ttctggtgag 20

<210> 399
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<400> 399
cgccttttct gaaaggtg 18

<210> 400
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attttctgca cagcagcg 18

<210> 401
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<223> downstream amplification primer for SEQ 226, SEQ 303

<400> 401
tattttctag ctcttctgg 19

<210> 402
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<223> downstream amplification primer for SEQ 227, SEQ 304

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agcaagagtg attgtaaag 19

<210> 403
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<223> downstream amplification primer for SEQ 228, SEQ 305

<400> 403
tattcagaaa ggagtggg 18

<210> 404
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SEQ 231, SEQ 308, SEQ 232, SEQ 309

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agagcgttct tgcctttc 18

<210> 405
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<400> 405
ggtaacccta aaatgttatc 20

<210> 406
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<400> 406
agaaaccata aggttatatt g 21

<210> 407
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<400> 407
acagtgcaaa gggttatatc 19

<210> 408
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<400> 408
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<210> 409
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<223> downstream amplification primer for SEQ 237, SEQ 314

<400> 409
gattccagaa gtccatttca g 21

<210> 410
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<223> downstream amplification primer for SEQ 238, SEQ 315

<400> 410
aggtaagaat gagcaaaaag g 21

<210> 411
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<210> 412
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<223> downstream amplification primer for SEQ 241, SEQ 318, SEQ 242, SEQ 319

<400> 412

cttgaaatac tcccagcc

18

<210> 413

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<223> downstream amplification primer for SEQ 243, SEQ 320, SEQ 244, SEQ 321, SEQ 245, SEQ 322, SEQ 246, SEQ 323, SEQ 247, SEQ 324, SEQ 248, SEQ 325, SEQ 249, SEQ 326

<400> 413

ccatgaactg agaactttg

19

<210> 414

<211> 18

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<223> downstream amplification primer for SEQ 250, SEQ 327

<400> 414

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18

<210> 415

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<222> 1..21

<223> downstream amplification primer for SEQ 251, SEQ 328

<400> 415

attcaggcac agaagtcata c

21

<210> 416

<211> 21

<212> DNA

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<222> 1..21
<223> downstream amplification primer for SEQ 252, SEQ 329, SEQ 253, SEQ 330

<400> 416
agggcagcac aatgtagtaa g 21

<210> 417
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<223> downstream amplification primer for SEQ 254, SEQ 331

<400> 417
cctctttatc tccaaacc 18

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<223> downstream amplification primer for SEQ 255, SEQ 332

<400> 418
gaaaacaatc aagctctgg 19

<210> 419
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<400> 419
cctttatatc cttggagtc 19

<210> 420
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<223> downstream amplification primer for SEQ 257, SEQ 334

<400> 420

tattacacgt tccaactctt c

21

<210> 421

<211> 20

<212> DNA

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<222> 1..20

<223> downstream amplification primer for SEQ 258, SEQ 335

<400> 421

ctgtgtttaa gtgactgctg

20

<210> 422

<211> 21

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<222> 1..21

<223> downstream amplification primer for SEQ 259, SEQ 336

<400> 422

ttattgcccc acatgcttga g

21

<210> 423

<211> 19

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<222> 1..19

<223> downstream amplification primer for SEQ 260, SEQ 337

<400> 423

tcattcgtct ggctaggtc

19

<210> 424

<211> 21

<212> DNA

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<220>

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<222> 1..21

<223> downstream amplification primer for SEQ 261, SEQ 338

<400> 424
gaaacagact gaagcaagga c 21

<210> 425
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<223> potential microsequencing oligo for 4-14-107.mis1

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acaaccacca aatgcatac 19

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<223> potential microsequencing oligo for 4-14-317.mis1

<400> 426
acatgcaagg tgggcaaga 19

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<400> 427
aacacagaaa ccgctaaaa 19

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<400> 428
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19

<210> 433

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<210> 434

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<210> 435

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<210> 436

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<210> 437
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tataaacaga aacatggatg agt 23

<210> 439
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atatagagtg tgcattccctg aca

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cctgagtcctc agggggctga cag 23

<210> 446
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ttttaaacaat tgatgaatct tta 23

<210> 447
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<210> 449

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tccatgtcat tattattcaa aag

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aatcatgcag agagaatgc

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19

<210> 458

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<222> 1..23

<223> microsequencing oligo for 4-58-289.mis1

<400> 458

catacctgca gcctgctttt ggt

23

<210> 459

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<223> microsequencing oligo for 4-58-318.mis1

<400> 459

tgactacttt acctgcaata ttt

23

<210> 460

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<223> microsequencing oligo for 4-60-266.mis1

<400> 460

aacaggacca agacactgca tta

23

<210> 461

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<400> 461
aagtttcagt atttcttagc aga

23

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aaaaaatagt gactgccac

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<210> 464
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tcaaatacagg acacaccac

19

<210> 465
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cccagaacat tcaccagct 19

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<210> 472
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<400> 472
cactgtgacc caggcgctag cgt 23

<210> 473
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<210> 474
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<400> 474
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<210> 475
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<400> 475
acactcatgt tagttagat 19

<210> 476
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<223> microsequencing oligo for 99-140-130.mis1

<400> 476
caaaagcagc tacagacca 19

<210> 477
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<400> 477

ttcaagggtta gtaactcat

19

<210> 478

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<223> potential microsequencing oligo for 99-147-181.mis1

<400> 478

catgaaaaag agcatgata

19

<210> 479

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<222> 1..19

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<400> 480

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<210> 481

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aaaatccact tgtaatcgc 19

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<400> 483
tatctataca aataatttt 19

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ctatacaaat aattttgaa 19

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<223> potential microsequencing oligo for 99-148-139.mis1

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aataattttg aatttaata 19

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